

9. (Amended) A host cell which produces a modified DNA polymerase having an amino acid sequence that shares not less than 95% homology to SEQ ID NO:4, which DNA polymerase during DNA sequencing effectively incorporated fluorescent dye-labeled dideoxynucleotide terminators ddCTP, ddATP, ddTTP and ddGTP, and has a reduction in the selective discrimination against incorporation of fluorescent dye-labeled dideoxynucleotide terminators ddCTP and ddATP,

B² wherein the DNA polymerase in its unmodified state has leucine, glutamate, and glutamate residues at positions 342-344, respectively, and a phenylalanine at position 422, the positions being determined based on a last lysine residue in the end of the sequence counted as position 588, wherein the DNA polymerase selectively discriminates against incorporation of fluorescent dye-labeled dideoxynucleotide terminators ddCTP and ddATP but does not discriminate against incorporation of fluorescent dye-labeled dideoxynucleotide terminators ddTTP and ddGTP.

29. (Amended) A DNA construct comprising:

- B³
- (i) a nucleotide sequence encoding a modified DNA polymerase which has an amino acid sequence that shares not less than 95% homology to a DNA polymerase isolated from a strain of *Bacillus stearothermophilus* (of *Bacillus caldotenax*, having an amino acid sequence that shares not less than 95% homology to SEQ ID NO:4, which nucleotide sequence encodes threonine, proline and leucine residues at positions 342-344, respectively, and a tyrosine residue at position 422, wherein the DNA polymerase in its unmodified state has leucine, glutamate, and glutamate residues at positions 342-344, respectively, and a phenylalanine at position 422, the positions being determined based on a last lysine residue in the end of the sequence counted as position 588; and
 - (ii) a vector, for introducing the DNA construct into eukaryotic and procaryotic host cells.